

Figure 2: Clone 7.7 is the homolog of human clone

## KIAA0313

- Clone 7.7 exhibits 75% identity and 95% similarity of human clone KIAA0313.

Clone7.7  
KIAA0313

GGKDVSAEAESSMVPVTTTEAKVPMPAHIAVTPSTTKGLIARKEGRYREPPPTPPGYV  
GGKDVSI EAESSLTSVTTEETKVPMPAHIAVASSTTKGLIARKEGRYREPPPTPPGYI  
\*\*\*\*\* \*\*\*\*\*. \*\*\*\*\*

Clone7.7  
KIAA0313

GGIPIADFEGPCHPARKPPDYNVALQSRMVARPTEAPAG--QTPP-AAAA\$RPGSKPQ  
GGIPIITDFEGH\$HPARKPPDYNVALQSRMVARSSDTAGPSSVQQPHGHTSSR\$RVNKPQ  
\*\*\*\*\* \*\*\*\*\* ..... \* \* \* \* \* \* \* \* \*

Clone7.7  
KIAA0313

WHKPSDADPRLAPFQAGFAGAEDEDEQVSAV (SEQ ID NO: 28)  
 WHKPNESDPRAPYQSQGFSTEDEDEQVSAV (amino acid nos. 1348 to 1499 of SEQ ID NO: 2)



4618 b.p.

1/1 31/11  
 atg aaa tca cta gca atc cca gct aac cat gga gtt atg ggc cag cag gag aaa cac tca  
 M K P L A I P A N H G V M G Q Q E K H S  
 61/21 91/31  
 ctt cct gca gat ttc aca aaa ctg cat ctt act gac agt ctc cac cca cag gtg acc cac  
 L P A D F T K L H L T D S L H P Q V T H  
 121/41 151/51  
 gtt tct tct agc cat tca gga tgt agt atc act agt gat tct ggg agc agc agt ctt tct  
 V S S S H S G C S I T S D S G S S S L S  
 181/61 211/71  
 gat atc tac cag gcc aca gaa agc gag gct ggt gat atg gac ctg agt ggg ttg cca gaa  
 D I Y Q A T E S E A G D M D L S G L P E  
 241/81 271/91  
 aca gca gtg gat tcc gaa gac gac gac gat gaa gaa gac att gag aga gca tca gat cct  
 T A V D S E D D D D E E D I E R A S D P  
 301/101 331/111  
 ctg atg agc agg gac att gtg aga gac tgc cta gag aag gac cca att gac cgg aca gat  
 L M S R D I V R D C L E K D P I D R T D  
 361/121 391/131  
 gat gac att gaa caa ctc ttg gaa ttt atg cac cag ttg cct gct ttt gcc aat atg aca  
 D D I E Q L L E F M H Q L P A F A N M T  
 421/141 451/151  
 atg tca gtg agg cga gaa ctc tgt gct gtg atg gtg ttc gca gtg gtg gaa aga gca ggg  
M S V R R E L C A V M V F A V V E R A G  
 481/161 511/171  
 acc ata gtg tta aat gat ggt gaa gag ctg gac tcc tgg tca gtg att ctc aat gga tct  
T I V L N D G E E L D S W S V I L N G S  
 541/181 571/191  
 gtg gaa gtg act tat cca gat gga aaa gca gaa ata ctg tgc atg gga aat agt ttt ggt  
V E V T Y P D G K A E I L C M G N S F G  
 601/201 631/211  
 gtc tct cct acc atg gac aaa gaa tac atg aaa gga gtg atg aga aca aag gtg gat gac  
V S P T M D K E Y M K G V M R T K V D D  
 661/221 691/231  
 tgc cag ttt gtc tgc ata gcc cag caa gat tac tgc cgt att ctc aat caa gta gaa aag  
C O F V C I A O O D Y C R I L N O V E K  
 721/241 751/251  
 aac atg caa aaa gtt gaa gag gaa gga gag att gtt atg gtg aaa gaa cac cga gaa ctt  
N M O K V E E E G E I V M V K E H R E L  
 781/261 811/271  
 gat cga act gga aca aga aag gga cac att gtc atc aag ggt acc tca gaa agg tta aca  
D R T G T R K G H I V I K G T S E R L T  
 841/281 871/291  
 atg cat ttg gtg gaa gag cat tca gta gta gat cca aca ttc ata gaa gac ttt ctg ttg  
M H L V E E H S V V D P T F I E D F L L  
 901/301 931/311  
 acc tat agg act ttt ctt tct agc cca atg gaa gtg ggc aaa aag tta ttg gag tgg ttt  
T Y R T F L S S P M E V G K K L L E W F  
 961/321 991/331  
 aat gac ccg agc ctc agg gat aag gtt aca cgg gta gta tta ttg tgg gta aat aat cac  
N D P S L R D K V T R V V L L W V N N H  
 1021/341 1051/351  
 ttc aat gac ttt gaa gga gat cct gca atg act cga ttt tta gaa gaa ttt gaa aac aat  
 F N D F E G D P A M T R F L E E F E N N

cNMP-BD

REM



1081/361 1111/371  
ctg gaa aga gag aaa atg ggt gga cac cta agg ctg ttg aat atc gcg tgt gct gct aaa  
L E R E K M G G H L R L L N I A C A A K  
1141/381 1171/391  
gca aaa aga aga ttg atg acg tta aca aaa cca tcc cga gaa gct cct ttg cct ttt atc  
A K R R L M T L T K P S R E A P L P F I  
1201/401 1231/411  
tta ctt gga ggc tct gag aag gga ttt gga atc ttt gtt gac agt gta gat tca ggt agc  
L L G G S E K G F G I F V D S V D S G S  
1261/421 1291/431  
aaa gca act gaa gca ggc ttg aaa cgg ggg gat cag ata tta gaa gta aat ggc caa aac  
K A T E A G L K R G D O I L E V N G Q N  
1321/441 1351/451  
ttt gaa aac att cag ctg tca aaa gct atg gaa att ctt aga aat aac aca cat tta tct  
F E N I O L S K A M E I L R N N T H L S  
1381/461 1411/471  
atc act gtg aaa acc aat tta ttt gta ttt aaa gaa ctt cta aca aga ttg tca gaa gag  
I T V K T N L F V F K E L L T R L S E E  
1441/481 1471/491  
aaa aga aat ggt gcc ccc cac ctt cct aaa att ggt gac att aaa aag gcc agt cgc tac  
K R N G A P H L P K I G D I K K A S R Y  
1501/501 1531/511  
tcc att cca gat ctt gct gta gat gta gaa cag gtg ata gga ctt gaa aaa gtg aac aaa  
S I P D L A V D V E Q V I G L E K V N K  
1561/521 1591/531  
aaa agt aaa gcc aac act gtg gga gga agg aac aag ctg aaa aag ata ctc gac aag act  
K S K A N T V G G R N K L K K I L D K T  
1621/541 1651/551  
cgg atc agt atc ttg cca cag aaa cca tac aat gat att ggg att ggt cag tct caa gat  
R I S I L P Q K P Y N D I G I G Q S Q D  
1681/561 1711/571  
gac agc ata gta gga tta agg cag aca aag cac atc cca act gca ttg cct gtc agt gga  
D S I V G L R Q T K H I P T A L P V S G  
1741/581 1771/591  
acc tta tca tcc agt aat cct gat tta ttg cag tca cat cat cgc att tta gac ttc agt  
T L S S S N P D L L Q S H H R I L D F S  
1801/601 1831/611  
gct act cct gac ttg cca gat caa gtg cta agg gtt ttt aag gct gat cag caa agc cgc  
A T P D L P D O V L R V F K A D Q Q S R  
1861/621 1891/631  
tac atc atg atc agt aag gac act aca gca aag gaa gtg gtc att cag gct atc agg gag  
Y I M I S K D T T A K E V V I O A I R E  
1921/641 1951/651  
ttt gct gtt act gcc acc ccg gat caa tat tca cta tgt gag gtc tct gtc aca cct gag  
F A V T A T P D O Y S L C E V S V T P E  
1981/661 2011/671  
gga gta atc aaa caa aga aga ctt cca gat cag ctt tcc aaa ctt gca gac aga ata caa  
G V I K O R R L P D O L S K L A D R I O  
2041/681 2071/691  
ctg agt gga agg tat tat ctg aaa aac aac atg gaa aca gaa act ctt tgt tca gat gaa  
L S G R Y Y L K N N M E T E T L C S D E  
2101/701 2131/711  
gat gct cag gag ttg ttg aga gag agt caa att tcc ctc ctt cag ctc agc act gtg gaa  
D A Q E L L R E S Q I S L L O L S T V E  
2161/721 2191/731  
gtt gca aca cag ctc tct atg cga aat ttt gaa ctc ttt cgc aac att gaa cct act gaa  
V A T O L S M R N F E L F R N I E P T E

PDZ

RA

Figure 3C



2221/741 2251/751  
tat ata gat gat tta ttt aaa ctc aga tca aaa acc agc tgt gcc aac ctg aag aga ttt  
Y I D D L F K L R S K T S C A N L K R F  
2281/761 2311/771  
gaa gaa gtc att aac cag gaa aca ttt tgg gta gca tct gaa att ctc aga gaa aca aac  
E E V I N Q E T F W V A S E I L R E T N  
2341/781 2371/791  
cag ctg aag agg atg aag atc att aag cat ttc atc aag ata gca ctg cac tgt agg gaa  
Q L K R M K I I K H F I K I A L H C R E  
2401/801 2431/811  
tgc aag aat ttt aac tca atg ttt gca atc atc agt ggc cta aac ctg gca cca gtg gca  
C K N F N S M F A I I S G L N L A P V A  
2461/821 2491/831  
aga ctg cga acg acc tgg gag aaa ctt ccc aat aaa tac gaa aaa cta ttt caa gat ctc  
R L R T T W E K L P N K Y E K L F O D L  
2521/841 2551/851  
caa gac ctg ttt gat cct tcc aga aac atg gca aaa tat cgt aat gtt ctc aat agt caa  
Q D L F D P S R N M A K Y R N V L N S Q  
2581/861 2611/871  
aat cta caa cct ccc ata atc cct cta ttc cca gtt atc aaa aag gat ctc acc ttc ctt  
N L O P P I I P L F P V I K K D L T F L  
2641/881 2671/891  
cac gaa gga aat gac tca aaa gta gac ggg ctg gtc aat ttt gag aag cta agg atg att  
H E G N D S K V D G L V N F E K L R M I  
2701/901 2731/911  
gca aaa gaa att cgt cac gtt ggc cga atg gct tca gtg aac atg gac cct gcc ctc atg  
A K E I R H V G R M A S V N M D P A L M  
2761/921 2791/931  
ttc agg act cgg aag aag aaa tgg cgg agt ttg ggg tct ctc agc cag ggt agt aca aat  
F R T R K K K W R S L G S L S Q G S T N  
2821/941 2851/951  
gca aca gtg cta gat gtt gct cag aca ggt ggt cat aaa aag cgg gta cgt cgt agt tcc  
A T V L D V A Q T G G H K K R V R R S S  
2881/961 2911/971  
ttt ctc aat gcc aaa aag ctt tat gaa gat gcc caa atg gct cga aaa gtg aag cag tac  
F L N A K K L Y E D A Q M A R K V K O Y  
2941/981 2971/991  
ctt tcc aat ttg gag cta gaa atg gac gag gag agt ctt cag aca tta tct ctg cag tgt  
L S N L E L E M D E E S L O T L S L Q C  
3001/1001 3031/1011  
gag cca gca acc aac aca ttg cct aag aat cct ggt gac aaa aag cct gtc aaa tcc gag  
E P A T N T L P K N P G D K K P V K S E  
3061/1021 3091/1031  
acc tct cca gta gct cca agg gca ggg tca caa cag aaa gct cag tcc ctg cca cag ccc  
T S P V A P R A G S Q Q K A Q S L P Q P  
3121/1041 3151/1051  
cag cag cag cca cca cca gca cat aaa atc aac cag gga cta cag gtt ccc gcc gtg tcc  
Q Q Q P P P A H K I N Q G L Q V P A V S  
3181/1061 3211/1071  
ctt tat cct tca cgg aag aaa gtg ccc gta aag gat ctc cca cct ttt ggc ata aac tct  
L Y P S R K K V P V K D L P P F G I N S  
3241/1081 3271/1091  
cca caa gct tta aaa aaa att ctt tct ttg tct gaa gaa gga agt ttg gaa cgt cac aag  
P Q A L K K I L S L S E E G S L E R H K  
3301/1101 3331/1111  
aaa cag gct gaa gat aca ata tca aat gca tct tgg cag ctt tct tct cct cct act tct  
K Q A E D T I S N A S S Q L S S P P T S

CDC25

Insertion  
Unique to  
GRF4

Continuation of the  
CDC25 domain

Figure 3D



3361/1121 3391/1131  
cca cag agt tct cca agg aaa ggc tat act ttg gct ccc agt ggt act gtg gat aat ttt  
P Q S S P R K G Y T L A P S G T V D N F  
3421/1141 3451/1151  
tca gat tct ggt cac agt gaa att tct tca cga tcc agt att gtt agc aat tct tct ttt  
S D S G H S E I S S R S S I V S N S S F  
3481/1161 3511/1171  
gac tca gtg cca gtc tca ctg cac gat gag agg cgc cag agg cat tct gtc agc atc gtg  
D S V P V S L H D E R R Q R H S V S I V  
3541/1181 3571/1191  
gaa aca aac cta ggg atg ggc agg atg gag agg cgg acc atg att gaa cct gat cag tat  
E T N L G M G R M E R R T M I E P D Q Y  
3601/1201 3631/1211  
agc ttg ggg tcc tat gca cca atg tcc gag ggc cga ggc tta tat gct aca gct aca gta  
S L G S Y A P M S E G R G L Y A T A T V  
3661/1221 3691/1231  
att tct tct cca agc aca gag gaa ctt tcc cag gat cag ggg gat cgc gcg tca ctt gat  
I S S P S T E E L S Q D Q G D R A S L D  
3721/1241 3751/1251  
gct gct gac agt ggc cgt ggg agc tgg acg tca tgc tca agt ggc tcc cat gat aat ata  
A A D S G R G S W T S C S S G S H D N I  
3781/1261 3811/1271  
cag acg atc cag cac cag aga agc tgg gag act ctt cca ttc ggg cat act cac ttt gat  
Q T I Q H Q R S W E T L P F G H T H F D  
3841/1281 3871/1291  
tat tca ggg gat cct gca ggt tta tgg gca tca agc agc cat atg gac caa att atg ttt  
Y S G D P A G L W A S S S H M D Q I M F  
3901/1301 3931/1311  
tct gat cat agc aca aag tat aac agg caa aat caa agt aga gag agc ctt gaa caa gcc  
S D H S T K Y N R Q N Q S R E S L E Q A  
3961/1321 3991/1331  
cag tcc cga gca agc tgg gcg tct tcc aca ggt tac tgg gga gaa gac tca gaa ggt gac  
Q S R A S W A S S T G Y W G E D S E G D  
4021/1341 4051/1351  
aca ggc aca ata aag cgg agg ggt gga aag gat gtt tcc att gaa gcc gaa agc agt agc  
T G T I K R R G G K D V S I E A E S S S  
4081/1361 4111/1371  
cta acg tct gtg act acg gaa gaa acc aag cct gtc ccc atg cct gcc cac ata gct gtg  
L T S V T T E E T K P V P M P A H I A V  
4141/1381 4171/1391  
gca tca agt act aca aag ggg ctc att gca cga aag gag ggc agg tat cga gag ccc ccg  
A S S T T K G L I A R K E G R Y R E P P  
4201/1401 4231/1411  
ccc acc cct ccc ggc tac att gga att ccc att act gac ttt cca gaa ggg cac tcc cat  
P T P P G Y I G I P I T D F P E G H S H  
4261/1421 4291/1431  
cca gcc agg aaa ccg ccg gac tac aac gtg gcc ctt cag aga tct cgg atg gtc gca cga  
P A R K P P D Y N V A L Q R S R M V A R  
4321/1441 4351/1451  
tcc tcc gac aca gct ggg cct tca tcc gta cag cag cca cat ggg cat ccc acc agc agc  
S S D T A G P S S V Q Q P H G H P T S S  
4381/1461 4411/1471  
agg cct gtg aac aaa cct cag tgg cat aaa ccg aac gag tct gac ccg cgc ctc gcc cct  
R P V N K P Q W H K P N E S D P R L A P

PY motifs

Figure 3E



4441/1481

4471/1491

tat cag tcc caa ggg ttt tcc acc gag gag gat gaa gat gaa caa gtt tct gct gtt tga  
Y Q S Q G F S T E E D E D E Q V S A V \*

4501/1501

4531/1511

**PDZ binding motif**

ggc aca gac ttt tct gga agc aga gcg agc cac ctg aaa gga gag cac aag aag acg tcc  
G T D F S G S R A S H L K G E H K K T S

4561/1521

4591/1531

tga gca ttg gag cct tgg aac tca cat tct gag gac ggt gga cca gtt tgc ctc ctt c  
\* A L E P W N S H S E D G G P V C L L

(SEQ ID NO: 1)

(SEQ ID NO: 2)

Figure 3F

[illegible]

### Figure 4

<b>hGRF4</b>	<b>TLSLQCEPATNT</b>	(SEQ ID NO: 2)
<b>dGRF4</b>	<b>RFSLECEPAHGS</b>	(SEQ ID NO: 7)
<b>hEpac</b>	<b>RLSRELEP----</b>	(SEQ ID NO:8)
<b>mRasGRF2</b>	<b>ELSLKIEPRLPA</b>	(SEQ ID NO: 9)
<b>dSOS</b>	<b>NESLRIEPRGCK</b>	(SEQ ID NO: 10)
<b>hRasGRP</b>	<b>ELSYAREPNRHR</b>	(SEQ ID NO: 11)



Figure 5:  
GRF4-REM domain

CDC25	-IRGGTKEALIEHLT-SHELVDAAFNVTMLITFRSILT-TREFFYALIIYRY-	(SEQ ID NO: 12)
Sos_mouse_	-IKGGTVVKLIERLT-YHMYADPNF-VRFTLTYSRFSCK-PQELNLLIERFE	(SEQ ID NO: 13)
RasGEF_aimless_	VVKFASLNKLVEHLT-HDSKHDLQFLKTFMLTYQSFT-PEKLMSKLQORY-	(SEQ ID NO: 15)
GRF2_mouse_	-IRYASVEALLERLT-DLRFLSIDFLNTFLHTYRIFTT-ATVVLAKLSDIY-	(SEQ ID NO: 14)
GRF4	-IKG-TSERLTMHLVEEHSVVDPTFIEDFLTYRTFLSSPMEVGKKLLEWFN	(SEQ ID NO: 2)
	:: : * : * . . . . . * :	





Figure 7

# PDZ domain

hGRF4	LTKPSREAPLPFILLGGSEK-----GFGIFVDSVDSGSKATEAG-LKRGDQIL	
dGRF4	LTRSSRDEPLNFRIVGGYELRGVAIATGNAAVGIYISHVEPGSKAQDVG-LKRGDQIH	
hPTP-BAS-1	NLKKDAKYGLGFQIIGGEKMGRL-----DLGIFISSVAPGGPADLDGCLKPGDRLI	
hPSD-95	IVIHGSTGLGFNIVGGEDG-----EGIFISFILAGGPADLSGELRKGDQIL	
rLin-7-C	VELPKTEEGLGFNIMGKEQ-----NSPIYISRIIPGGIADRHGGLKRGDQLL	
hDGL	VKVQKGSEPLGISIVSGEKG-----GIYVSKVTVGSIAHQAG-LEYGDQLL	
	. * : : : * .	* : : : * . * . * . * .

13/34

hGRF4	EVNGQNFENIQLSKAMEILR	(SEQ ID NO: 2)
dGRF4	EVNGQSLDHVTSKRALEILT	(SEQ ID NO: 16)
hPTP-BAS-1	SVNSVSLEGVSHHAAIEILQ	(SEQ ID NO: 17)
hPSD-95	SVNGVDLRNASHEQAIALK	(SEQ ID NO: 18)
rLin-7-C	SVNGVSVEGEHHEKAVELLK	(SEQ ID NO: 19)
hDGL	EFNGINLRSATEQQARLIIG	(SEQ ID NO: 20)
	... * . . .	





Figure 9:

## GRF4-RA domain

dgk-1a\_ce\_

GRF4

RaIGDS\_h\_

```

-----REDFE---IIRVFDGNN---YRSQIS-----RNIVVAKHVSQVQRDAALR
--HHRILDFS---ATPDLPDQVLRVFKADQQS-----RYIMISKDTTAKVVTQAIR
SILVTSQDKAPSVISRVLKKNRDSAVASEYELVQLLPGERELTIPASANVFYAMDGASH
*
: : : : :
: : : : :

```

dgk-1a\_ce\_

GRF4

RaIGDS\_h\_

```

RFHI--NDTPERYIT-QVWGEVEEILED---PVP-----LRNVKRPPEGKRAQIFIR
EFAV--TATPDQYSLC-EVSVTPEGVIKQR-----RLP-----DQLSK--LADRIQLSGR
DFLLRHGEGPLLLHLASFVARLPQELLRVREEGAPFFGSRPQGGRLHGHCSSEEAPLAYR
* : * : * : * :

```

dgk-1a\_ce\_

GRF4

RaIGDS\_h\_

(SEQ ID NO: 26)

(SEQ ID NO: 2)

(SEQ ID NO: 27)

YYD-----

YYLKNNME--

SHGVHTRCG

:



6568 bp

/translation="MKPLAIPANHGVMGQEQKHSLPADFTKLHLTDSLHPQVTHVSSS  
HSGCSITSDSGSSSLSDIYQATESEAGMDLGLPETA VDSEDDDDDEEDIERASDPLM  
SRDIVRDCLEKDPIDRTDDIEQLLEFMHQLPAFANMTMSVRRELCAVMVFAVVERAG  
TIVLNDGEELDSWSVILNGSVEVTYPDGKAEILCMGNSFGVSPMTDKEYMKGMVMTKV  
DDCQFVCIAQQDYCRILNQVEKNMQKVEEAGEIVMVKEHRELDRTGTRKGHIVIKGTS  
ERLTMHLVEEHSVVDPTFIEDFLTYRTFLSSPMEVGKKLLEWFNDPSLRDKVTRVVL  
LWVNNHFNDFEGDPAMTRFLEEFENNLEREKMGHRLRLNIACAAKAKRRLMTLTKPS  
REAPLPFILLGGSEKGFIFVDSVDSGSKATEAGLKRGDQILEVNGQNFENIQLSKAM  
EILRNNTLSITVKTNLVFKELLTRLSEEKRNAGPHLPKIGDIKKASRYSIPDLAVD  
VEQVIGLEKVNKSKANTVGGRNKLKKILDKTRISILPQKPYNDIGIGQSQDDSIIVGL  
RQTKHIPTALPVSGTLSSSNPDLLQSHHRLDFSATPDLPDQVLRVFKADQQSRYIMI  
SKDTTAKENVVIAIREFAVTA TPDQYSLCEVSVTPEGVIKQRRLPDQLSKLADRIQLS  
GRYYLKNNMETELTCSDEDAQELLRESQISLLQLSTVEVATQLSMRNFELEFRNIEPTE  
YIDDLFKLRSKTSCANLKRFEVINQETFWVASEILRETNQLKRMKIIKHFIKIALHC  
RECKNFNSMFAIISGLNLAPVARLRTTWEKLPNKYEKLFQDLQDLFDPSRNMAYKRN  
LNSQNLQPPHLPFVKKDLTFLHEGNDKVDGLVNFELRMIAKEIRHVGRMASVN  
MDPALMFRTRKKKWRSLGSLSQGSTNATVLDVAQTGGHKKRVRSSFLNAKKLYEDAQ  
MARKVKQYLSNLEEMDEESLQTLSQLCEPATNTLPKNPGDKKPVKSETSPVAPRAGS  
QKKAQSLPQPQQPPPAHKINQGLQVPAVSLYPSRKKVPVKDLPPFGINSQALKKIL  
SLSEEGSLERHKKQAEDTISNASSQLSSPPTSPQSSPRKGYTLAPSGTVDNFSDSGHS  
EISSRSSIVSNSSFDSVPVSLHDERRQRHSVSIVETNLGMGRMERRTMIEPDQYSLGS  
YAPMSEGRGLYATATVISSPSTEELSQQDQDRASLDAADSGRGSWTS CSSGSHDNIQT  
IQHQRSWETLPFGHTHFDYSGDPAGLWASSSHMDQIMFSDHSTKYNRQNSRESLEQA  
QSRASWASSTGYWGEDSEGDTGTIKRRGGKDVSI EAESSLTSVTTEETKPVMPMAHI  
AVASSTTKGLIARKEGRYREPPPTPPGYIGIPITDFPEGHSHPARKPPDYNVALQRSR  
MVARSSDTAGPSSVQQPHGHPTSSRPVNKPQWHPKNESDPRAPYQSQGFSTEDEDE  
QVSAV" | SEQ ID NO: 2]

63. .4562

BASE COUNT 1974 a 1400 c 1463 g 1731 t  
ORIGIN

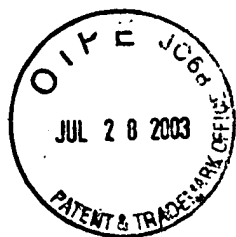
1 cttgccatcg tgagagattg gtacatgatg tgtaaatca gttcagcata tgtttctca  
61 ttatgaaacc actagcaatc ccagctaacc atggagttat gggccagcag gagaacact  
121 cacttctgc agatttcaca aaactgcac tcactgacag tctccacca caggtgacct  
181 acgtttctc tagccattca ggatgtagta tcactagtga ttctgggagc agcagtctt  
241 ctgatatcta ccagggccaca gaaagcgagg ctggtgatat ggacctgagt ggggtgccag  
301 aaacagcagt ggattccgaa gacgacgacg atgaagaaga cattgagaga gcatcagatc  
361 cctgatgag cagggaact gtgagagact gcctagagaa ggacccaatt gaccggacag  
421 atgatgacat tgaacaactc ttggaattta tgcaccagtt gcctgcttt gccaatatga  
481 caatgtcagt gaggcgagaa cctgtgtctg tgatggtgtt cgcagtgtg gaaagagcag  
541 ggaccatagt gttaatgat ggtgaagagc tggactcctg gtcagtgtt ctcaatggt  
601 ctgtggaagt gacttatcca gatggaaaag cagaaatact gtgcatggga aatagtgtt  
661 gtgtctctcc taccatggac aaagaataca tgaaggagat gatgagaaca aaggtggatg  
721 actgccagtt tgtctgcata gccagcaag attactgccg tatttcaat caagtagaaa  
781 agaactgca aaaagttgaa gaggaaggag agattgtat ggtgaagaa caccgagaac  
841 ttgatcgaac tggacaaga aaggacaca ttgtcatca ggttacctca gaaaggttaa  
901 caatgcattt ggtggaagag cattcagtag tagatccaac attcatagaa gactttctgt  
961 tgacctatag gactttctt tctagcccaa tggagtggtg caaaaagtt tggagtggt  
1021 ttaatgacct gagctcagg gataaggta cagggttagt attattgtg gtaataatc  
1081 acttcaatga cttgaagga gatcctgcaa tgactcgatt tttagaagaa ttgaaaaca  
1141 atctggaaag agagaaaatg ggtggacacc taaggctgtt gaatatcgcg tgtgtgcta  
1201 aagcaaaaag aagattgatg acgttaaca aaccatcccg agaagctcct ttgctttta  
1261 tcttacttg aggtctgag aagggtttg gaatctttgt tgacagtga gattcagga  
1321 gcaagcaac tgaagcaggc ttgaaacggg gggatcagat attagaagta aatggccaaa  
1381 accttgaaa cattcagctg tcaaaagcta tggaaattct tagaataaac acacatttat

Figure 19a



1441 ctatcactgt gaaaaccaat ttattgtat taaagaact tctaacaaga ttgtcagaag  
 1501 agaaaagaaa tgggtccccc cacttccta aaattggtga cattaaaaag gccagtgcgt  
 1561 actccattcc agatcttct gtatgttag aacaggtgat aggacttgaa aaagtgaaca  
 1621 aaaaaagtaa agccaacact gtggaggaa ggaacaagct gaaaaagata ctgcacaaga  
 1681 ctggatcag tatcttgcca cagaaacct acaatgatat tgggattgt cagtctcaag  
 1741 atgacagcat agtaggatta aggcagacaa agcacatccc aactgcattg cctgtcagt  
 1801 gaaccttatc atccagtaat cctgatttat tgcagtcaca tcatcgatt ttagacttca  
 1861 gtgctactcc tgaactgcca gatcaagtgc taagggttt taaggctgat cagcaaagcc  
 1921 gctacatcat gatcagtaag gacactacag caaagggaat ggctaticag gctatcagg  
 1981 agttgtctgt tactgccacc ccggatcaat attcactatg tgaggctctc gtcacacctg  
 2041 agggagtaat caaacaaga agacttcag atcagcttc caaactgca gacagaatac  
 2101 aactgagtgg aaggtattat ctgaaaaaca acatggaaac agaaactcti tttcagatg  
 2161 aagatgctca ggagttgtg agagagagtc aaatttccct ccttcagctc agcactgttg  
 2221 aagtgcaac acagctctct atgcgaaatt ttgaactct tgcgaacatt gaacctactg  
 2281 aatatataga tgatttatt aaactcagat caaaaaccag ctgtgccaac ctgaagagat  
 2341 ttgaagaagt cattaacag gaaacattt gggtagcatc tgaattctc agaaaaaca  
 2401 accagctgaa gaggatgaag atcattaagc atticatcaa gatagcactg cactgtagg  
 2461 aatgcaagaa tttaactca atgttgcaa tcatcagtgg cctaaacctg gcaccagtgg  
 2521 caagactcgc aacgacctgg gaaaaactc ccaataata cgaaaaacta ttcaagatc  
 2581 tccaagacct gttgatcct tccagaaaca tggcaaaata tctaatgti ctcaatagt  
 2641 aaaatctaca acctccata atccctctat tccagttat caaaaaggat ctacacctc  
 2701 ttcacgaagg aaatgactca aaagttagac ggctgggtcaa tttgagaag ctaaggatga  
 2761 ttgcaaaaga aattcgtcac gttggccgaa tggcttcagt gaacatggac cctgccctca  
 2821 tttcaggac tgggaagaag aaatggcgga gttggggtc tctcagccag ggtagtacaa  
 2881 atgcaacagt gctatgtgt gctcagacag gtgtcataa aaagcgggta cgtcgtagt  
 2941 cctttctcaa tgcacaaaag cttatgaag atgcccacat ggctcgaana gtgaagcagt  
 3001 accttccaa ttggagcta gaaatggac agagagagct tcaacatta tcttgcagt  
 3061 gtgagccagc aaccaacaca ttgcctaaga atcctgtga caaaaagcct gtcacatccg  
 3121 agacctcctc agtagctcca agggcagggt cacaacagaa agctcagtc ctgccacag  
 3181 ccagcagca gccaccacca gcacataaaa tcaaccaggg actacaggt cccgcctgt  
 3241 cctttatcc ttcacggaag aaagtgcctg taaaggatct cccactttt ggcataaact  
 3301 ctccacaagc tttaaaaaa attcttctt tgtctgaaga aggaagtgtg gaacgtcac  
 3361 agaaacaggc tgaagataca atataaatg catcttcgca gctttctct cctctactt  
 3421 ctccacagag ttctccaagg aaaggctata cttggctcc cagtgttact gtggataatt  
 3481 ttacagattc tggtcacagt gaaattctt cagatccag tattgttagc aattcgtct  
 3541 ttgactcagt gccagtctca ctgcacgat agaggcgcca gaggcattct gtcagatcg  
 3601 tggaaaacaa cctagggatg ggcaggatgg agaggcggac catgattgaa cctgatcagt  
 3661 atagcttggg gtctatgca ccaatgtcc agggccgagg ctatattgt acagctacag  
 3721 taattcttc tccaagcaca gaggaactt cccaggatca gggggatcgc gcgtcactg  
 3781 atgctgctga cagtggcctg gggagctgga cgtcatgctc aagtggctcc catgataata  
 3841 tacagacgat ccagcaccag agaagctggg agactctcc attcgggcat actcactttg  
 3901 attattcagg ggtatctgca gtttatggg catcaagcag ccatatggac caaattatg  
 3961 ttctgatca tagcacaag tataacaggc aaatcaaaag tagagagagc ctgaaacaag  
 4021 cccagtcctc agcaagctgg gcgtcttcca caggttactg gggagaagac tcagaagggt  
 4081 acacaggcac aataaagcgg aggggtggaa aggatgttc cattgaagcc gaaagcagta  
 4141 gcctaacgtc tgtgactac gaagaaacca agcctgtccc catgctgtcc cacatagctg  
 4201 tggcatcaag tactacaaag gggctcattg cagaaagga gggcagggtat cgagagcccc  
 4261 cgccccccc tccggctac attggaattc cctatttga ctttcagaa gggcactccc  
 4321 atccagccag gaaaccgctg gactacaag tggcccttca gagatcgcg atggtcgac  
 4381 gatcctccga cacagctggg cctcatccg tacagcagcc acatgggcat cccaccagca  
 4441 gcaggcctgt gaacaaacct cagtggcata aaccgaacga gtctgacctg cgcctcgccc  
 4501 ctatcagtc ccaagggtt tccaccagg aggatgaaga tgaacaagt tctgtgttt

Figure 19b



4561 gaggcacaga cttttctgga agcagagcga gccacctgaa aggagagcac aagaagacgt  
 4621 cctgagcatt ggagccttg aactcacatt ctgaggacgg tggaccagtt tgcctcctc  
 4681 cctgccttaa aagcagcatg gggtctctc tccctctct ccttccctt tgcattgta  
 4741 aatactgtga agaaattgcc ctggcacttt icagactttg ttgcttgaaa tgcacagtgc  
 4801 agcaatcttc gagctccac tgttctgcc tggcacatca cacagtatca ttccaaattc  
 4861 caagatcatc acaacaagat gattcactct ggctgcactt ctcaatgcct ggaaggattt  
 4921 ttttaactc tcttttaga ttcaatcca gtcttagcac ttgatctcat tgggataatg  
 4981 agaaaagcta gccattgaac tacttggggc cttaaccca ccaaggaga caaagaaaaa  
 5041 caatgaaac ctttagtac agtctgttc cactgtta caatgtcctc ctttaaaaa  
 5101 aaaaaatgag ttaaaagatt ttgtcagag agtaaatata tatccattat atgattacag  
 5161 tattattta aaccttaagt aggttgcca gcctgggtc tgaanaacca aatatgccg  
 5221 acagggtgtg gccacacca gaagacggga agacctggct tgtaccctg gcttcccatg  
 5281 tcttctggt ctacccgcg aagtgccta tcttggaagt atgaaatgt agcaattaa  
 5341 taccaagaca cctcatctgc tcttcccca gtggatgggg tcttctgta aaactgtttg  
 5401 cacatggcca ggggagggaa ctaggacctt tgtctctgt ctgagccta tggaggcagg  
 5461 acggtgtcat tggcggatgt gtcctgtcc atgagatgg atggcaaac ccattttaa  
 5521 gttatattc ttgatttt gttattag aggttaggt ttgtttt gttttgtt  
 5581 tttttaag agaaacattt ataactgat agcattgcag tgaagcagc ttgggatgtt  
 5641 ggagctaag ccagctgtt atactgtct tcaagacag cctccctta tgaattggc  
 5701 attaggaat aaacaagcct taaacgtga taaagatca aaacctggt tagacatgcc  
 5761 agccttgca aggcaggta gtaccaaag actaacctcc aagtggctt atggacgtg  
 5821 catatagaga aggcctaagt gtaccaaag actaacctcc aagtggctt atggacgtg  
 5881 gactgaaatg accctccac tctattttg tgtgtttg cacagactcc ggaagatga  
 5941 aggtgcca tctgagtagt actcaaatgt gaggaactgc tggcttga ttttttcc  
 6001 attaaattca gctgatcata ttgatcagta gataaacgta aatagcttca aatttaaaa  
 6061 gtggaattgc agtgtttt cactgtatca acaatgtca gtgctttatt taataattct  
 6121 ctctgtatc atggcattg tctactgtc tattacattg tcaattatgc atttgaatt  
 6181 ttacatgta tatgcattat ttgccagtt tattatatag gctatggacc tcatgtgcat  
 6241 atagaaagac agaaatctag ctctaccaca agtgacaa atgttatcta agcattaagt  
 6301 aatttagaa cataggactg ctatctcag ttcgtctgt gatgtcaagt gcagaatga  
 6361 caattactg gtgatttct catactttg atactactg tactgtatg tcttttagaa  
 6421 agacattgtt ggagtctga tccctttgt attttaata caataattgt acataatgt  
 6481 tatattttg ttgaagatgg tagaaatga ctatgttat gcttctacat ccagtttga  
 6541 caagctggaa aataaataaa tataacat [SEQ ID NO: 1]

Figure 19c



801 b.p.

1/1  
 ACT AAA GGG AAC AAA AGC TGG AGC TCC ACC GCG GTG GCG GCC GCT CTA GAA CTA GTG GAT  
 T K G N K S W S S T A V A A A L E L V D  
 L K G T K A G A P P R W R P L \* N \* W I  
 \* R E Q K L E L H R G G G R S R T S G S

31/11  
 61/21  
 CCC CCG GGC TGC AGG AAT TGA AGC GGT GGG AAG GAT GTC TCC GCT GAG GCA GAG AGC AGC  
 P P G C R N S S G G K D V S A E A E S S  
 P R A A G I Q A V G R M S P L R Q R A A  
 P G L Q E F K R W E G C L R \* G R E Q Q

91/31  
 121/41  
 AGC ATG GTG CCC GTG ACT ACA GAG GAA GCC AAA CCT GTC CCT ATG CCT GCC CAC ATA GCT  
 S M V P V T T E E A K P V P M P A H I A  
 A W C P \* L Q R K P N L S L C L P T \* L  
 H G A R D Y R G S Q T C P Y A C P H S C

151/51  
 181/61  
 GTG AGC CCG AGC ACT ACC AAG GGA CTC ATC GCA CGG AAG GAA GGC AGG TAC CGG GAG CCG  
 V T P S T T K G L I A R K E G R Y R E P  
 \* R R A L P R D S S H G R K A G T G S R  
 D A E H Y Q G T H R T E G R Q V P G A A

211/71  
 241/81  
 CCT CCC ACA CCT CCA GGC TAC GTG GGC ATC CCC ATT GCC GAT TTC CCA GAA GGG CCT TGC  
 P P T P P G Y V G I P I A D F P E G P C  
 L P H L Q A T W A S P L P I S Q K G L A  
 S H T S R L R G H P H C R F P R R A L P

271/91  
 301/101  
 CAC CCG GCC AGG AAG CCC CCG GAT TAC AAC GTG GCC CTG CAG CGG TCC CGC ATG GTG GCA  
 H P A R K P P D Y N V A L Q R S R M V A  
 T R P G S P R I T T W P C S G P A W W H  
 P G Q E A P G L Q R G P A A V P H G G T

331/111  
 361/121  
 CCG CCC ACT GAG GCC CCG GCA CCG GGC CAG ACG CCG CCT GCA GCC GCA GCC AGC CCG CCG  
 R P T E A P A P G Q T P P A A A A S R P  
 G P L R P R H R A R R R L Q P Q P A G R  
 A H \* G P G T G P D A A C S R S Q P A G

391/131  
 421/141  
 GGC AGC AAG CCA CAG TGG CAC AAG CCC AGC GAC GCA GAC CCA CGC CTC GCG CCC TTC CAG  
 G S K P Q W H K P S D A D P R L A P F Q  
 A A S H S G T S P A T Q T H A S R P S S  
 Q Q A T V A Q A Q R R R P T P R A L P A

451/151  
 481/161  
 CCG CAG GCT TCG CAG GAG CCG AGG AGG ACG AAG ATG AAC AAG TGT CTG CTG TTT GAG GCG  
 P Q A S Q E R R R T K M N K C L L F E A  
 R R L R R S G G G R R \* T S V C C L R R  
 A G F A G A E E D E D E Q V S A V \* G A

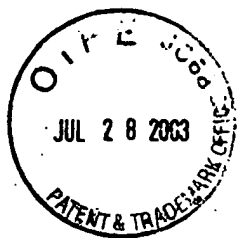
511/171  
 541/181  
 CAG GCT CCT TGA TCC ACA GTG AGC CAC CCA AAG GAG AGC ACA AGA AGA CGT CCC AAG CCT  
 Q A P \* S T V S H P K E S T R R R P K P  
 R L L D P Q \* A T Q R R A Q E D V P S L  
 G S L I H S E P P K G E H K K T S Q A L

571/191  
 601/201  
 TGG AGC CTT GGC ACG CAC ATC TGA GGA TGG TGG ACC AGT TTG CCT CCT TCC CTG CCT TAA  
 W S L G T H I \* G W W T S L P P S L P \*  
 G A L A R T S E D G G P V C L L P C L K  
 E P W H A H L R M V D Q F A S F P A L K

631/211  
 661/221  
 AGC AGC ATG GGG CTT CTT CTC CCC TTC TTT CCT TTT CAT GTG AAA TAC TGT GAA  
 S S M G L L L P F F L S P L H V K Y C E  
 A A W G F F S P S S F P L C M \* N T V K  
 Q H G A S S P L L P F P F A C E I L \* R

691/231

Figure 19d



721/241  
GAA ATT GCC CTG GCA CTT TGC AGA CTT GTT GCT TGA AAT GCA CAG CCC AGC AGC CCC TGA  
E I A L A L C R L V A . N A Q P S S P .  
K L P W H P A D L L L E M H S P A A P E  
N C P G T L Q T C C L K C T A Q Q P L S  
751/251  
781/261  
GCT GCT GCC TGC CAC GTC ACG [SEQ ID NO: 3]  
A A A C H V T [SEQ ID NO: 4]  
L L P A T S [SEQ ID NO: 5]  
C C L P R H [SEQ ID NO: 6]

FIGURE 19E